



SEQUENCE LISTING

<110> COEN, LAURENT
PINZOLAS, ROSARIO OSTA
BRULET, PHILIPPE

<120> HYBRID PROTEINS THAT MIGRATE RETROGRADELY AND
TRANSYNAPTICALLY INTO THE CNS

<130> 03495.0174-01000

<140> 09/816,467

<141> 2001-03-26

<150> 60/055,615

<151> 1997-08-14

<150> 60/065,236

<151> 1997-11-13

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 1600

<212> DNA

<213> Clostridium tetani

<220>

<221> CDS

<222> (88)..(1476)

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aagctggagc tcggtaccgc ggccacc atg gtt ttt tca aca cca att cca ttt 114
Met Val Phe Ser Thr Pro Ile Pro Phe
1 5

tct tat tct aaa aat ctg gat tgt tgg gtt gat aat gaa gaa gat ata 162
Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile
10 15 20 25

gat gtt ata tta aaa aag agt aca att tta aat tta gat att aat aat 210
Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn
30 35 40

gat att ata tca gat ata tct ggg ttt aat tca tct gta ata aca tat 258
Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr
45 50 55

cca gat gct caa ttg gtg ccc gga ata aat ggc aaa gca ata cat tta 306
Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu
60 65 70

09216467.062901

gta aac aat gaa tct tct gaa gtt ata gtg cat aaa gct atg gat att	354
Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile	
75 80 85	
gaa tat aat gat atg ttt aat aat ttt acc gtt agc ttt tgg ttg agg	402
Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg	
90 95 100 105	
ggt cct aaa gta tct gct agt cat tta gaa caa tat ggc aca aat gag	450
Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu	
110 115 120	
tat tca ata att agc tct atg aaa aaa cat agt cta tca ata gga tct	498
Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser	
125 130 135	
ggg tgg agt gta tca ctt aaa ggt aat aac tta ata tgg act tta aaa	546
Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys	
140 145 150	
gat tcc gcg gga gaa gtt aga caa ata act ttt agg gat tta cct gat	594
Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp	
155 160 165	
aaa ttt aat gct tat tta gca aat aaa tgg gtt ttt ata act att act	642
Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr	
170 175 180 185	
aat gat aga tta tct tct gct aat ttg tat ata aat gga gta ctt atg	690
Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met	
190 195 200	
gga agt gca gaa att act ggt tta gga gct att aga gag gat aat aat	738
Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn	
205 210 215	
ata aca tta aaa cta gat aga tgt aat aat aat aat caa tac gtt tct	786
Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser	
220 225 230	
att gat aaa ttt agg ata ttt tgc aaa gca tta aat cca aaa gag att	834
Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile	
235 240 245	
gaa aaa tta tac aca agt tat tta tct ata acc ttt tta aga gac ttc	882
Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe	
250 255 260 265	
tgg gga aac cct tta cga tat gat aca gaa tat tat tta ata cca gta	930
Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val	
270 275 280	
gct tct agt tct aaa gat gtt caa ttg aaa aat ata aca gat tat atg	978
Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met	
285 290 295	

Met Val Phe Ser Thr Pro Ile Pro Phe Ser Tyr Ser Lys Asn Leu Asp
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Cys Trp Val Asp Asn Glu Glu Asp Ile Asp Val Ile Leu Lys Lys Ser
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 Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser
 35 40 45
 Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro
 50 55 60
 Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu
 65 70 75 80
 Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn
 85 90 95
 Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser
 100 105 110
 His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met
 115 120 125
 Lys Lys His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys
 130 135 140
 Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg
 145 150 155 160
 Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala
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 Asn Lys Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala
 180 185 190
 Asn Leu Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly
 195 200 205
 Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg
 210 215 220
 Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe
 225 230 235 240
 Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr
 245 250 255
 Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr
 260 265 270
 Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val
 275 280 285
 Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser
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 Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly
 305 310 315 320

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Leu Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn Glu Ile Asp Ser
 325 330 335
 Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val Ser Tyr Asn Asn
 340 345 350
 Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe Asn Asn
 355 360 365
 Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly Ile Pro Leu
 370 375 380
 Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu Lys Thr Tyr Ser
 385 390 395 400
 Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser Leu Gly Leu Val
 405 410 415
 Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn Arg Asp Ile Leu
 420 425 430
 Ile Ala Ser Asn Trp Tyr Phe Asn His Leu Lys Asp Lys Ile Leu Gly
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<212> DNA

<213> Clostridium tetani

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 aatgatatta tatcagatat atctggggtt aattcatctg taataacata tccagatgct 180
 caattggtgc ccggaataaa tggcaaagca atacatttag taaacaatga atcttctgaa 240
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 agcttttggt tgagggttcc taaagtatct gctagtcatt tagaacaata tggcacaat 360
 gagtattcaa taattagctc tatgaaaaaa catagtctat caataggatc tggttggagt 420
 gtatcactta aaggaataaa cttaatatgg actttaaaag attccgcggg agaagttaga 480
 caaataactt ttagggattt acctgataaa tttaatgctt atttagcaaa taaatgggtt 540
 tttataacta ttactaatga tagattatct tctgctaatt tgtatataaa tggagtactt 600
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 aaactagata gatgtaataa taataatcaa tacgtttcta ttgataaatt taggatattt 720
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 tttttaagag acttctgggg aaacccttta cgatatgata cagaatatta tttaataacca 840
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 ggtatccctc tttataaaaa aatgggaagca gtaaaattgc gtgattttaa aacctattct 1200
 gtacaactta aattatatga tgataaaaat gcactcttag gactagtagg taccataat 1260

ggTcaaataG gcaacgatcc aaatagggat atattaattg caagcaactg gtactttaat 1320
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
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<210> 6
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<223> Description of Artificial Sequence: Primer

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27

<211> 41

<213> Artificial Sequence

<223> Description of Artificial Sequence: Primer

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<211> 12

<213> Unknown Organism

<223> Description of Unknown Organism: Construct
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<211> 12

<213> Unknown Organism

<223> Description of Unknown Organism: Construct
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<211> 24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Primer

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<210> 13
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 <212> DNA
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<220>
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<210> 15
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 <212> DNA
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 <223> Description of Artificial Sequence: Primer

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 <212> DNA
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<220>
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<220>
 <223> Description of Artificial Sequence: Linker

17

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14